

Table S8: Protein disorder abundance for disorder regions > 80 residues.

Organism ^a	%long80" ^b		
	MD ^c	IUPred ^c	NORSnet ^c
Thermophiles			
<i>Thermosynechococcus elongatus</i> BP-1	1.8 ± 0.5	0.9 ± 0.3	1.1 ± 0.4
<i>Clostridium clariflavum</i> DSM 19732	2.6 ± 0.5	0.8 ± 0.2	0.7 ± 0.2
<i>Streptococcus thermophilus</i> LMG 18311	2.8 ± 0.6	0.8 ± 0.3	0.7 ± 0.2
Hyperthermophiles			
<i>Aeropyrum pernix</i> K1	0.5 ± 0.3	0.1 ± 0.1	0.06 ± 0.1
<i>Pyrococcus horikoshii</i> OT3	0.7 ± 0.4	0.05 ± 0.09	1.2 ± 0.4
Psychrophiles			
<i>Desulfotalea psychrophila</i> LSv54	2.0 ± 0.4	0.8 ± 0.3	0.5 ± 0.2
<i>Colwellia psychrerythraea</i> 34H	1.9 ± 0.4	0.6 ± 0.2	0.5 ± 0.2
<i>Shewanella woodyi</i> ATCC 51908	2.3 ± 0.4	0.7 ± 0.2	0.6 ± 0.2
Psychrotolerants			
<i>Methanococcoides burtonii</i> DSM 6242	1.8 ± 0.5	0.7 ± 0.3	0.4 ± 0.2
<i>Leuconostoc citreum</i> KM20	3.0 ± 0.7	1.4 ± 0.5	0.9 ± 0.4
<i>Bacillus weihenstephanensis</i> KBAB4	2.4 ± 0.4	1.2 ± 0.3	0.6 ± 0.2
<i>Rhodoferax ferrireducens</i> T118	2.6 ± 0.4	0.8 ± 0.2	0.9 ± 0.3
Halophiles			
<i>Haloarcula marismortui</i> ATCC 43049	4.0 ± 0.6	5.3 ± 0.6	1.9 ± 0.4
<i>Halobacterium</i> sp. NRC-1	3.6 ± 0.7	3.9 ± 0.7	1.5 ± 0.5
<i>Marinobacter aquaeolei</i> VT8	3.5 ± 0.5	1.8 ± 0.4	0.9 ± 0.3
Alkalophile			
<i>Bacillus halodurans</i> C-125	2.2 ± 0.4	0.8 ± 0.3	0.3 ± 0.1
Radiation resistant			
<i>Deinococcus deserti</i> VCD115	2.0 ± 0.4	2.3 ± 0.5	1.3 ± 0.4
<i>Deinococcus maricopensis</i> DSM 21211	1.7 ± 0.4	1.8 ± 0.4	1.0 ± 0.3
<i>Deinococcus radiodurans</i>	3.0 ± 0.6	3.2 ± 0.6	1.9 ± 0.5
Taxonomic neighbors (mesophiles)			

<i>Caulobacter vibrioides</i>	3.2 ± 0.5	2.5 ± 0.5	1.8 ± 0.4
<i>Chromobacterium violaceum</i> ATCC 12472	2.8 ± 0.4	1.8 ± 0.4	1.4 ± 0.3
<i>Clostridium acetobutylicum</i>	1.8 ± 0.4	0.4 ± 0.2	0.2 ± 0.1
<i>Corynebacterium glutamicum</i>	3.1 ± 0.5	2.7 ± 0.5	1.9 ± 0.4
<i>Desulfovibrio vulgaris</i> str. Hildenborough	3.0 ± 0.5	3.1 ± 0.5	1.3 ± 0.3
<i>Geobacter metallireducens</i> GS-15	2.5 ± 0.5	1.1 ± 0.3	1.0 ± 0.3
<i>Geobacter sulfurreducens</i> PCA	2.4 ± 0.5	1.2 ± 0.3	1.1 ± 0.3
<i>Lactococcus lactis</i> subsp. <i>lactis</i> II1403	3.0 ± 0.7	1.2 ± 0.4	0.8 ± 0.3
<i>Listeria innocua</i>	2.5 ± 0.5	0.8 ± 0.3	0.3 ± 0.2
<i>Methanosa</i> cina mazei Go1	2.4 ± 0.5	1.3 ± 0.4	0.9 ± 0.3
<i>Methanococcus maripaludis</i> S2	1.5 ± 0.5	0.3 ± 0.3	0.3 ± 0.2
<i>Nitrosomonas europaea</i> ATCC 19718	2.2 ± 0.6	0.9 ± 0.4	0.7 ± 0.3
<i>Pseudoalteromonas atlantica</i> T6c	2.1 ± 0.4	1.0 ± 0.3	0.7 ± 0.2
<i>Rhodopseudomonas palustris</i> CGA009	3.6 ± 0.5	2.6 ± 0.4	2.0 ± 0.4
<i>Rhodospirillum rubrum</i> ATCC 11170	3.1 ± 0.5	1.9 ± 0.4	1.6 ± 0.4
<i>Rhodobacter sphaeroides</i> 2.4.1	2.8 ± 0.5	2.2 ± 0.4	1.4 ± 0.3
<i>Shewanella oneidensis</i>	2.5 ± 0.4	0.8 ± 0.2	0.7 ± 0.2
<i>Ruegeria pomeroyi</i> DSS-3	1.6 ± 0.4	1.2 ± 0.3	0.6 ± 0.2
<i>Streptomyces coelicolor</i>	4.2 ± 0.4	5.9 ± 0.5	3.4 ± 0.4
<i>Synechococcus elongatus</i> PCC 6301	2.2 ± 0.5	1.0 ± 0.4	1.3 ± 0.4
<i>Synechocystis</i> sp. PCC 6803 substr. Kazusa	2.7 ± 0.5	1.7 ± 0.4	1.4 ± 0.4
Eukaryotes			
<i>Arabidopsis thaliana</i>	17.1 ± 0.4	10.5 ± 0.3	17.2 ± 0.4
<i>Caenorhabditis elegans</i>	17.9 ± 0.5	15.5 ± 0.4	18.3 ± 0.5
<i>Dictyostelium discoideum</i>	23.6 ± 0.7	24.4 ± 0.7	18.8 ± 0.6
<i>Drosophila melanogaster</i>	27.5 ± 0.7	25.6 ± 0.7	28.3 ± 0.7
<i>Schizosaccharomyces pombe</i> 972h-	21 ± 1	12.6 ± 0.8	18 ± 1
<i>Saccharomyces cerevisiae</i> S288c	22.1 ± 0.9	16.0 ± 0.8	$19.7 \pm 0.$

- a. Organism marks the full name of the organism where grey cells correspond to the environments; Taxonomic neighbors correspond to organisms that are related in phylogeny to the extremophiles described in this study. Eukaryotes picked at random from the set of completely sequenced organisms in UniProt.

- b. Disorder %long80 refers to the percentage of proteins in a proteome that contains at least one region with ≥ 80 consecutive residues predicted as disordered.
- c. <MD | IUPred | NORSnet> refer to the three prediction methods used, in order to catch the different “flavors” of disorder.